Construction of a Kinematic Variable Sensitive to the Mass of the Standard Model Higgs Boson in

 $H o WW^* o \ell^+ \nu \ell^- \bar{\nu}$ using Symbolic Regression

Suyong Choi

Department of Physics Korea University, Seoul 136-713 Republic of Korea

 $E ext{-}mail:$ suyong@korea.ac.kr

ABSTRACT: We derive a kinematic variable that is sensitive to the mass of the Standard Model Higgs boson (M_H) in the $H \to WW^* \to \ell^+ \nu \ell^- \bar{\nu}$ channel using symbolic regression method. Explicit mass reconstruction is not possible in this channel due to the presence of two neutrinos which escape detection. Mass determination problem is that of finding a mass-sensitive function that depends on the measured observables. We use symbolic regression, which is an analytical approach to the problem of non-linear regression, to derive an analytic formula sensitive to M_H from the two lepton momenta and the missing transverse momentum. Using the newly-derived mass-sensitive variable, we expect Higgs mass resolutions between 1 to 4 GeV for M_H between 130 and 190 GeV at the LHC with 10 fb^{-1} of data. This is the first time symbolic regression method has been applied to a particle physics problem.

Keywords: Higgs boson, Mass, Symbolic Regression, LHC.

Contents

1.	Introduction	1
2.	Mass Reconstruction in $H \to WW^* \to \ell^+ \nu \ell^- \bar{\nu}$	1
3.	Symbolic Regression and Application to M_H Reconstruction	2
	3.1 Symbolic Regression	
	3.2 Symbolic Regression Applied to $H \to WW^* \to \ell^+ \nu \ell^- \bar{\nu}$	4
	3.3 Mass Sensitivity of S_{mass} variable at LHC	6
4.	Conclusions	7

1. Introduction

In light of the current limits on the Standard Model (SM) Higgs boson mass (M_H) , $H \to WW^* \to \ell^+ \nu \ell^- \bar{\nu}$ channel is expected to be one of the most important channels in the search for the Higgs boson [1, 2, 3, 4]. Direct search results at the CERN LEP e^+e^- collider places a lower limit of 114.4 GeV on M_H at 95% confidence level (C.L.) [1]. And indirect constraints obtained from fits to precision electroweak data, when combined with direct searches at LEP, place an upper bound of 157 GeV at 95% C.L. [4]. In this mass range, the branching fraction of $H \to WW$ is sizable and the production of $gg \to H$ through top quark loop has the largest cross section for both the Tevatron and the LHC energies [5]. Discovery of the Higgs boson and measurement of its properties are important for completing the picture of electroweak symmetry breaking mechanism. However, measurement of mass in $H \to WW^*$ is not trivial.

2. Mass Reconstruction in $H \to WW^* \to \ell^+ \nu \ell^- \bar{\nu}$

In the $H \to WW^* \to \ell^+ \nu \ell^- \bar{\nu}$ channel, there are two neutrinos which escape detection. The system is underconstrained and it is not possible to determine the momenta of the two neutrinos. Typical analyses in these channels involve selection criteria on simple kinematic variables, and cross section upper limits are derived using the distributions of dilepton azimuthal opening angle which reflects the spin 0 nature of the Higgs boson [2, 3]. To increase the sensitivity of the searches and to measure the mass, it is desirable to have a variable that has direct information on the mass of the Higgs boson (M_H) .

There are a couple of kinematic variables that can be used for mass reconstruction in the $H \to WW^* \to \ell^+ \nu \ell^- \bar{\nu}$ channel [6, 7]. They are either generalizations of transverse mass (M_T) or modifications of solutions to kinematic problems in supersymmetric (SUSY) models. These variables show linear behavior to M_H and are sensitive to it. While these variables are motivated by kinematics of the event, it is not clear in what sense these variables are optimal.

We approach the problem of M_H measurement from a different perspective. Since the kinematics of an event reflects M_H , we should be able to extract M_H from the leptons and missing transverse momenta which contain the maximal information. We would like to construct a function such that, on average, $\langle F(\vec{x}(m)) \rangle = m$, where \vec{x} are the measured quantities from a detector. Since there are infinitely many such functions, some optimization condition is necessary to arrive at an optimal function. This is a problem of non-linear multivariate regression.

There are advanced analyses techniques which allow us to construct a multivariate function $\hat{F}(\vec{x})$ that can be regarded as an approximation to the ideal function $F(\vec{x})$ [8]. A function is built from a training data set such that $\hat{F}(\vec{x}) \approx F(\vec{x})$. Its performance can be evaluated on a test sample, from variance or some other measure of error. However, most of these methods are black boxes, such that if we write down the solution, we would not be able to make much sense of it. Also, these methods are not able to generalize sufficiently and undesired biases show up for data sample close to the boundaries of input variables. Instead, we take an analytic approach to function approximation called symbolic regression.

3. Symbolic Regression and Application to M_H Reconstruction

3.1 Symbolic Regression

In a symbolic regression, a function which minimizes certain criteria (or maximizes fitness) is constructed from the input variables analytically [9, 10]. Symbolic regression is an application of genetic programming methodology and genetic algorithms. Symbolic regression methods are powerful enough to derive invariants, such as Hamiltonian, from a set of experimental data with non-linearities [11]. An advantage of symbolic regression is its interpretability, in contrast to purely numerical methods.

Genetic algorithms are often employed in problems of optimization with many parameters. It is an application of natural evolution to computational domain. In a genetic algorithm, a set of individuals form a population, where an individual is represented by a gene. Each position in a gene can be used to encode some strategy or functionality. Behavior of an individual, also known as phenotype, is determined by its genetic constitution or genotype. The fitness of an individual is evaluated at the level of phenotype.

If two individuals with different genotypes show the same phenotype, then they have identical fitness. Fitness is a measure of how well an individual achieves the desired goal. In genetic algorithms of computational domains, fitness is explicitly defiend, unlike the biological world, where fitness is implicit.

Evolution of population is achieved through genetic operations which create new genotypes or modify existing ones. Cross-over and mutation operations are genetic operators that can be used to create individuals for successive generations. Cross-over operation (sexual reproduction) is applied to a pair of parent genes to create a child gene. An individual can also undergo a point mutation (asexual reproduction) in a gene. Local minima in the fitness landscape can be avoided because of this randomness. Strength of genetic algorithm approach comes from the randomness of the genetic operations and the variety of genes present in a population. Genetic algorithms are finding their way into high energy physics in optimization problems [12, 13]. For this study, we created our own genetic algorithm package to overcome the limitations of existing tools.

Symbolic regression is a method that can be applied to problems where we want to map input variables to the output. It arrives at the answer using genetic algorithms. In a symbolic regression, analytic equations form the population. An individual is usually encoded as an expression binary tree (Fig. 1), but other representations are possible. A linear encoding would make the genes look closer to their biological counterpart, but this is not necessary. Evaluation of fitness and manipulation of the genes are much more efficient in a binary tree representation. Internal nodes of a binary tree are operators or functions and terminal nodes

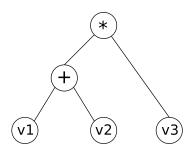


Figure 1: A binary tree of expression (v1 + v2) * v3.

are either numerical constants or variables. Set of operators, variables, constants, and fitness function or minimization criteria must be defined for each problem.

An initial population is built randomly from a given set of operators, variables and constants. Individuals of subsequent generations are created by applying either gene cross-over operations to a pair of "father" and "mother" equations to yield a "child" equation (Fig. 2) or through mutation on existing expressions. Selection of parents can vary among implementations. In this study, each parent is selected through tournaments. A tournament is held among a small randomly selected pool from the population and the best-fit individual is chosen. Through tournaments, fitter individuals have a greater chance to pass on parts of the genes.

Point mutation operation is applied to each individual nodes randomly with small probability. This is independent of the sexual reproduction. Point mutation mimics random mutations that occur in biological processes. The effect of mutation is diversification of the gene pool. Although random mutations may make the individual less fit, it may still be beneficial when an offspring inherits some of the mutations.

At each generation, individuals are sorted according to their fitness and those with poor fitness are discarded by keeping the population size constant. The best fit individuals ("the elite") are passed along to the next generation without modification, but they can participate in sexual reproduction. The number of generations or termination criteria has to be decided upon as a parameter of the algorithm. The details of implementation are discussed in detail elsewhere [14].

In a more traditional method of optimization, a minimum is reached by descending the fitness landscape in a smooth manner through incremetal changes. In a genetic algorithm, genetic operations introduce local changes in the genes, but the behavior of the child can be quite different (Fig 2). It is understood that fitness landscape can be probed more globally with genetic algorithms. Maintaining genetic diversity is crucial to the success

since genetic algorithms can still be trapped in local minima if there is not much genetic diversity. Applying a strong selection pressure on the population, such as having a large fraction of the population participating in a tournament, is not necessarily beneficial since it can effectively reduce the genetic pool to that of a few fit individuals.

Physical dimensions of resulting formulae of symbolic regression may not be correct. This is also true of traditional multivariate regression algorithms. However, in a symbolic regression, we can control the terms that can appear in an expression. In this study, we created dimensionally constrained symbolic regression (DCSR) where only terms that are dimensionally correct can appear. For example, in a DCSR, terms like $p_x + p_y^3/(p_x \cdot p_z)$ can present, but not $p_x + p_y^3$. In a DCSR, cross over operations can only occur among branches with the same physical dimension.

In tests of simple problems where we know the optimal answer, such as mass

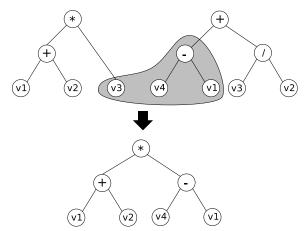


Figure 2: Creation of a child through cross-over operation. The cross over of genes occurring between v3 and v4 - v1 from the two parents yields a new child (v1 + v2) * (v4 - v1).

determination in $W \to \ell \nu$, DCSR, as well as the normal symbolic regression, is able to arrive at an equation that differs from the well-known transverse mass (M_T) by a multiplicative factor. However, for more complicated problems, solutions of DCSR converge much more rapidly. And in some cases, only DCSR produces satisfactory solutions.

3.2 Symbolic Regression Applied to $H \to WW^* \to \ell^+ \nu \ell^- \bar{\nu}$

Higgs mass determination in $H \to WW^* \to \ell^+ \nu \ell^- \bar{\nu}$ in hadron colliders is an inportant problem. In this channel, two lepton momenta $\vec{p}_{\ell 1}, \vec{p}_{\ell 2}$ and the vector sum of the two neutrino transverse momenta $\vec{E}_T = \vec{E}_{T\nu 1} + \vec{E}_{T\nu 2}$ are measured in experiments. Since there are only two equations related to neutrino momenta, the system is under-constrained. If we knew both W bosons were real, we would still need two extra equations to constrain the system. Therefore one cannot solve for the neutrino momenta exactly even in principle.

Existing studies relied on analysis of kinematics to find expressions that behave linearly to the Higgs boson mass [6, 7]. In this study, we approach the problem as that of finding an expression that not only shows linear behavior, but also whose widths of the mass distribution are narrow.

Symbolic regression is applied to a data generated with PYTHIA $pp \to H \to WW^* \to \ell^+ \nu \ell^- \bar{\nu}$ at $\sqrt{s} = 14$ TeV with M_H varying from 120 GeV to 200 GeV [15]. Detector simulation is not applied to the data. Momentum components and energy of the two charged leptons $(p_{1T}, p_{1x}, p_{1y}, p_{1z}, E_1, p_{2T}, p_{2x}, p_{2y}, p_{2z}, E_2)$ and missing E_T information $(\not\!E_T, \not\!E_x, \not\!E_y)$ are used as input variables for the symbolic regression. The fitness function used is the average of fractional absolute difference: $\frac{1}{N} \sum_i |M_{rec,i} - M_{H,i}|/M_{H,i}$.

Without DCSR, the symbolic regression is not able to yield meaningful results. This seems to be due to the larger number of variables used. The number of terms of dimension 2 with only multiplication allowed is 78. In our implementation, four basic arithmetic operators $(+, -, \times, \div)$ and transcendental functions (sin, cos, log, exp) are allowed, which makes the number of possible terms infinite.

If fractional root mean-squared (RMS) $(\frac{1}{N}[\sum_i (M_{rec,i} - M_{H,i})^2/M_{H,i}^2]^{1/2})$ were used as the fitness function, the symbolic regression would get trapped into local minima even with DCSR. This is consistent with what is known about genetic algorithms since outliers pay a heavy penalty with such a fitness function. Overall, it has the effect of reducing the diversity.

Figure 3 shows evolution of fitness of best-fit individuals in 100 runs as a function of the number of generations. DCSR is able to converge on meaningful results and yields the best estimate for the M_H^2 as

$$S_{mass}^2 = 2p_{1T}^2 + 2p_{2T}^2 + 3\left(p_{1T}p_{2T} + \cancel{E}_T(p_{1T} + p_{2T}) - \cancel{E}_T \cdot (\vec{p}_{1T} + \vec{p}_{2T}) - 2\vec{p}_{1T} \cdot \vec{p}_{2T}\right).$$

Symmetry of the two leptons in the system is recognized by the symbolic regression automatically, even though symmetry condition was not imposed.

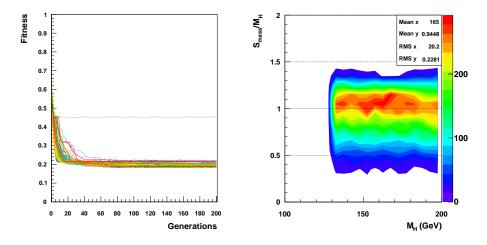


Figure 3: Left: Evolution of best fit individuals function in 100 runs. Right: Distribution of ratio of predicted mass to true mass, m_{pred}/m_H , versus the true Higgs mass m_H . The sample was generated using PYTHIA.

For a Higgs of $M_H = 160$ GeV which decays to two real W bosons, if the charged leptons both travel in the same direction, transverse to the beam with 0 longitudinal momentum components, $S_{mass} = \frac{5}{4}M_H$. The other extreme case, where $\vec{E}_T = 0$ and the two lepton momenta are opposite to each other in the transverse plane, $S_{mass} = \frac{1}{4}M_H$. Other configurations of lepton momenta and \vec{E}_T yields different values of S_{mass} . Since we are assuming perfect knowledge on lepton momenta and \vec{E}_T , the width of the distribution reflects the fact that some of the information on two neutrinos is irretrevably lost. The distribution of S_{mass} shows good fractional RMS (Fig. 4). Mass resolution depends not

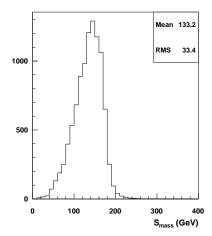


Figure 4: Distribution of reconstructed mass for $S_{mass}(\text{top})$ for $M_H = 140 \text{ GeV}$ for pp collisions at $\sqrt{s} = 14 \text{ TeV}$.

only on the RMS but also on the shape of the distribution, and this is described in a latter section under more realistic conditions. By replacing $p_{1T}p_{2T}$ with $2p_{1T}p_{2T}$ in S_{mass} , one can get a variable with the mean closer to M_H , but its distribution is wider.

Since the simulated data used to derive the equation was from pp collision at $\sqrt{s} = 14$ TeV, it is worth to look at how S_{mass} would perform for a different scenario, such as Tevatron where $p\bar{p}$ collides at $\sqrt{s} = 1.96$ TeV. The Higgs bosons at the Tevatron are expected to be produced with a smaller boost and the kinematics of the final state particles are different. Fortunately, even in this case, the S_{mass} variables shows linearity and similar fractional RMS (Fig. 5). Therefore, we conclude that S_{mass} captures genuine features of $H \to WW^* \to \ell^+ \nu \ell^- \bar{\nu}$ system.

3.3 Mass Sensitivity of S_{mass} variable at LHC

Sensitivity of a variable to mass depends on the shape of the mass distributions for the signals. In order to study the sensitivity of the mass variables under a more realistic conditions, we generated $pp \to H \to WW^* \to \ell^+ \nu \ell^- \bar{\nu}$ events at $\sqrt{s}=14$ TeV using MadEvent generator with PGS v4 detector simulation and reconstruction [16]. We assume $pp \to WW^*$ and $pp \to t\bar{t}$ as backgrounds. We generated the simulated signal samples in the mass range between 120 GeV/ c^2 and 200 GeV/ c^2 at 2.5 GeV/ c^2 intervals. Both the signal and background samples are scaled to the NLO cross sections by applying appropriate K-factors [17, 18, 19].

The selection critera are as follows:

- Two leptons of $p_T > 15$ GeV and $|\eta| < 2.5$
- 12 GeV $< M_{\ell\ell} < 300 \text{ GeV}$
- $E_T > 30 \text{ GeV}$

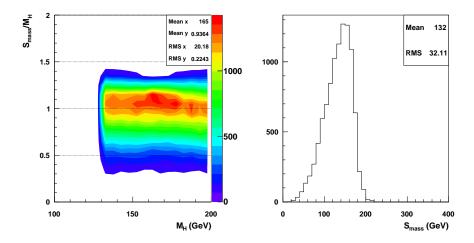


Figure 5: Left: the linearity of the S_{mass} in $p\bar{p} \to H \to WW^* \to \ell^+\nu\ell^-\bar{\nu}$ at Tevatron energies $\sqrt{s} = 1.96$ TeV. Right: S_{mass} distribution for $M_H = 140$.

- $M_{T2} > 50 \text{ GeV}$
- $|\Delta\phi_{\ell\ell}| < 1.8$
- No hadronic jets with $p_T > 20 \text{ GeV}$

The last 3 critera reduce the $t\bar{t}$ backgrounds significantly and WW^* backgrounds moderately. The M_{T2} variable is a good variable to use, since signal-to-background increases [7]. The S_{mass} variable is weakly correlated with the M_{T2} variable, and for larger values of M_{T2} , the S_{mass} distribution becomes sharper. The selection has the effect of removing events with smaller values of S_{mass} where backgrounds are copious. The S_{mass} distributions for various values of M_H are shown in Fig. 6.

To take into account theoretical and experimental uncertainties, 10% uncertainty in the overall normalization is assumed. To evaluate the uncertainties in mass determination, templates of signal and backgrounds S_{mass} distributions are used to conduct pseudo-experiments. Log-likelihood is calculated for each mass hypothesis and then fitted with a parabola to extract the mass resolutions (Fig. 7). The mass resolution is obtained from the parabola when $-\ln \mathcal{L}/\mathcal{L}_{max} = \frac{1}{2}$ (Fig. 8). Mass resolution improves from 3.7 GeV to 1.3 GeV as on-shell decay of Higgs becomes possible. With M_H dependent cuts on $\Delta \phi_{\ell\ell}$ and M_{T2} , the mass resolution improves slightly [7]. The S_{mass} variable is correlated with other mass variables for $H \to WW$, but the correlation is not 100%. Therefore, further improvement may be possible by forming suitable combinations of the variables.

4. Conclusions

Symbolic regression is used to derive a kinematic variable which is sensitive to the mass of the Higgs boson in the $H \to WW^* \to \ell^+ \nu \ell^- \bar{\nu}$ channel at hadron colliders. With this

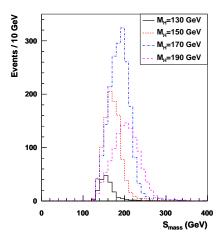


Figure 6: S_{mass} distributions of the Higgs signal for various M_H expected in 10 fb^{-1} at LHC after event selection.

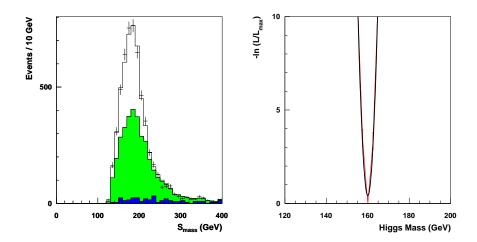
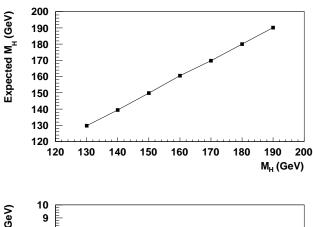


Figure 7: Left: Template histograms of $t\bar{t}$ (dark), WW^* (light), and $H \to WW^*$ with $M_H = 140$ GeV (white) for $10fb^{-1}$. The error bars show what a typical data would look like. Right: Log-likelihood as a function of mass for a 160 GeV Higgs.

variable, the mass of the Higgs boson can be measured with an accuracy of 1 to 4 GeV in the Higgs mass range between 130 GeV and 190 GeV at the LHC with 10 fb^{-1} of data. This is the first time symbolic regression method has been applied to high-energy physics problem.

Acknowledgments

This work has been supported by Junior Investigator Grant (2009-0069251) of the Korean National Research Foundation (NRF).



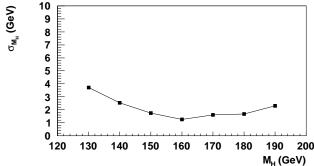


Figure 8: Linearity (top) and mass resolution (bottom) expected as obtained from pseudo-experiments in 10 fb^{-1} for pp collisions at $\sqrt{s} = 14$ TeV,

$M_H ext{ (GeV)}$	130	140	150	160	170	180	190
11 \	3.7						
σ_{M_H} (GeV) optimized	3.7	2.4	1.7	0.8	1.2	1.5	1.8

Table 1: Expected Higgs mass resolutions using S_{mass} variable with 10 fb^{-1} data in pp collisions at $\sqrt{s} = 14$ TeV. The last row shows mass resolutions expected for mass-dependent optimized analyses.

References

- [1] R. Barate et al., Phys. Lett. **B** 565 (2003) 61.
- [2] T. Aaltonen et al., Phys. Rev. Lett. 104 (2010) 061803.
- [3] V. Abazov et al., Phys. Rev. Lett. 104 (2010) 061804.
- [4] The LEP Electroweak Working Group, the Tevatron Electroweak Working Group, the SLD electroweak and heavy flavour groups, arXiv:0911.2604.
- [5] T. Han, A.S. Turcot, and R-J. Zhang, Phys. Rev. D 59 (1999) 093001; M. Carena et al. (Higgs Working Group Collaboration), hep-ph/0010338.
- [6] Alan J. Barr, Ben Gripaios, Christopher Gorham Lester, J. High Energy Phys. 0907 (2009) 072.
- [7] Kiwoon Choi, Suyong Choi, Jae Sik Lee, Chan Beom Park, Phys. Rev. D 80 (2009) 073010.

- [8] T. Hastie, R. Tibshirani, J. Friedman, 2001. The Elements of Statistical Learning; Data Mining, Inference, and Prediction, Springer-Verlag.
- [9] Holland, John H. 1975. Adaptation in Natural and Artificial Systems, University of Michigan Press.
- [10] J. R. Koza, 1992. Genetic Programming: On the Programming of Computers by Means of Natural Selection, Cambridge, MA: MIT Press.
- [11] M. Schmidt and Hod Lipson, Science **324** (2009) 81.
- [12] S. Abdullin, et al., hep-ph/0605143.
- [13] http://root.cern.ch
- [14] In preparation.
- [15] Torbjörn Sjöstrand, Stephen Mrenna and Peter Skands, J. High Energy Phys. **0605** (2006) 026.
- [16] J. Alwall et al., J. High Energy Phys. 0709 (2007) 028.
- [17] V. Ravindran, J. Smith, W.L. van Neerven, Nucl. Phys. B 665 (2003) 325.
- [18] T. Binoth, M. Ciccolini, N. Kauer, M. Krmer, J. High Energy Phys. 0503 (2005) 065.
- [19] S. Catani, M.L. Mangano, P. Nason, L. Trentadue, Phys. Lett. B 378 (1996) 329.